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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,217

DATE: 06/08/2001
TIME: 14:47:04

Input Set : C:\PAOLA\09828217.txt
Output Set: N:\CRF3\06082001\I828217.raw

SEQUENCE LISTING

ENTERED

- 4 (1) GENERAL INFORMATION:
6 (i) APPLICANT: HIRANO, TOSHIO
7 KAISHO, TSUNEYASU
9 (ii) TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING
10 PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF
12 (iii) NUMBER OF SEQUENCES: 2
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
16 P.C.
17 (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
18 (C) CITY: ARLINGTON
19 (D) STATE: VA
20 (E) COUNTRY: USA
21 (F) ZIP: 22202
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/828,217
C--> 31 (B) FILING DATE: 09-Apr-2001
32 (C) CLASSIFICATION:
41 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 09/182,563
36 (B) FILING DATE:
38 (A) APPLICATION NUMBER: PCT/JP94/01732
39 (B) FILING DATE: 14-OCT-1994
42 (A) APPLICATION NUMBER: JP 5-281622
43 (B) FILING DATE: 15-OCT-1993
45 (viii) ATTORNEY/AGENT INFORMATION:
46 (A) NAME: OBLON, NORMAN F.
47 (B) REGISTRATION NUMBER: 24,618
48 (C) REFERENCE/DOCKET NUMBER: 7625-001-0 PCT
50 (ix) TELECOMMUNICATION INFORMATION:
51 (A) TELEPHONE: 703-413-3000
52 (B) TELEFAX: 703-413-2220
55 (2) INFORMATION FOR SEQ ID NO: 1:
57 (i) SEQUENCE CHARACTERISTICS:
58 (A) LENGTH: 180 amino acids
59 (B) TYPE: amino acid
60 (C) STRANDEDNESS: single
61 (D) TOPOLOGY: linear
63 (ii) MOLECULE TYPE: peptide
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly

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71 1 5 10 15
73 Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
74 20 25 30
76 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
77 35 40 45
79 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
80 50 55 60
82 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
83 65 70 75 80
85 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
86 85 90 95
88 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
89 100 105 110
91 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
92 115 120 125
94 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
95 130 135 140
97 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
98 145 150 155 160
100 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
101 165 170 175
103 Ala Leu Leu Gln
104 180

106 (2) INFORMATION FOR SEQ ID NO: 2:

108 (i) SEQUENCE CHARACTERISTICS:
109 (A) LENGTH: 996 base pairs
110 (B) TYPE: nucleic acid
111 (C) STRANDEDNESS: double
112 (D) TOPOLOGY: linear

114 (ii) MOLECULE TYPE: cDNA to mRNA
119 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

121 GTGGAATTCA	TGGCATCTAC	TTCGTATGAC	TATTGCAGAG	TGCCCATGGA	AGACGGGGAT	60
123 AAGCGCTGTA	AGCTTCTGCT	GGGGATAGGA	ATTCTGGTGC	TCCTGATCAT	CGTGATTCTG	120
125 GGGGTGCCCT	TGATTATCTT	CACCATCAAG	GCCAACAGCG	AGGCCTGCCG	GGACGGCCCTT	180
127 CGGGCAGTGA	TGGAGTGTG	CAATGTCAACC	CATCTCCTGC	AACAAGAGCT	GACCGAGGCC	240
129 CAGAAGGGCT	TTCAGGATGT	GGAGGCCAG	GCCGCCACCT	GCAACCACAC	TGTGATGGCC	300
131 CTAATGGCTT	CCCTGGATGC	AGAGAAGGCC	CAAGGACAAA	AGAAAGTGG	GGAGCTTGAG	360
133 GGAGAGATCA	CTACATTAAA	CCATAAGCTT	CAGGACGCGT	CTGCAGAGGT	GGAGCGACTG	420
135 AGAAGAGAAA	ACCAGGTCTT	AAGCGTGAGA	ATCGCGGACA	AGAAAGTACTA	CCCCAGCTCC	480
137 CAGGACTCCA	GCTCCGCTGC	GGCGCCCCAG	CTGCTGATTG	TGCTGCTGG	CCTCAGCGCT	540
139 CTGCTGCAGT	GAGATCCCAG	GAAGCTGGCA	CATCTTGGAA	GGTCGTCCT	GCTCGGCTTT	600
141 TCGCTTGAAC	ATTCCCTTGA	TCTCATCAGT	TCTGAGCGGG	TCATGGGGCA	ACACGGTTAG	660
143 CGGGGAGAGC	ACGGGGTAGC	CGGAGAAGGG	CCTCTGGAGC	AGGTCTGGAG	GGGCCATGGG	720
145 GCAGTCCTGG	GTGTGGGGAC	ACAGTCGGGT	TGACCCAGGG	CTGTCTCCCT	CCAGAGCCTC	780
147 CCTCCGGACA	ATGAGTCCCC	CCTCTTGTCT	CCCACCCCTGA	GATTGGGCAT	GGGGTGCGGT	840
149 GTGGGGGGCA	TGTGCTGCCT	GTTGTTATGG	GTTCCTTTTG	CGGGGGGGT	TGCTTTTTC	900
151 TGGGGTCTTT	GAGCTCCAAA	AAATAAACAC	TTCCCTTGAG	GGAGAGCAA	AAAAAAA	960
153 AAAAAAAAAA	AAAAAAAAAA	AAAGAATTCC	ACCACAA			996

VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]